Applicant: Ricardo Azpiroz et al.

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## Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

## Listing of Claims:

## 1.-16. (Cancelled).

- 17. (Currently Amended) A method of modulating a DWF4 polypeptide comprising:
- (a) providing a host cell, wherein said host cell comprises a recombinant vector, said recombinant vector comprising:
  - (i) an isolated dwf4 polynucleotide, wherein said isolated dwf4 polynucleotide comprises a sequence having at least 50% 85% identity to a complement of SEQ ID NO:1[[,]] and complements and reverse complements segments thereof; and
  - (ii) a control element operably linked to said isolated dwf4-polynucleotide, whereby a coding sequence within said isolated dwf4 polynucleotide can be transcribed and translated in said host cell; and
- (b) culturing said host cell under conditions whereby said isolated dwf4 polynucleotide is transcribed, wherein whereby expression of dwf4 said DWF4 polypeptide is inhibited.
- 18.-35. (Cancelled).
- 36. (Currently Amended) A method for producing a transgenic plant having an altered phenotype relative to a corresponding wild-type plant comprising:

introducing an isolated dwf4 polynucleotide into a plant cell, wherein said isolated dwf4 polynucleotide comprises a sequence having at least 50% 85% identity to a complement of SEQ ID NO:1[[,]] and complements and reverse complements segments thereof; and

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producing a transgenic plant from said plant cell, said transgenic plant having an altered phenotype relative to the wild-type plant, wherein the isolated dwf4-polynucleotide inhibits expression of dwf4 said DWF4 polypeptide.

37. (Currently Amended) A method for producing a transgenic plant having an altered phenotype relative to a corresponding wild-type plant comprising:

introducing first and second isolated dwf4 polynucleotides into a plant cell, wherein said first and second isolated dwf4-polynucleotides independently comprise a sequence having at least 50% 85% identity to a complement of SEQ ID NO:1[[,]] and complements and reverse complements segments thereof; said first and second isolated dwf4-polynucleotides operably linked to at least first and second tissue-specific promoters, wherein said first isolated dwf4 polynucleotide is overexpressed and wherein said second isolated dwf4-polynucleotide inhibits expression of dwf4 said DWF4 polypeptide; and

producing a transgenic plant from said plant cell, said transgenic plant having an altered phenotype relative to the wild-type plant.

38.-57. (Cancelled).

- 58. (New) The method of claim 17, wherein said sequence having at least 85% sequence identity to a complement of SEQ ID NO:1 is at least 100 nucleotides long.
- 59. (New) The method of claim 58, wherein said sequence having at least 85% sequence identity to a complement of SEQ ID NO:1 is at least 200 nucleotides long.
- 60. (New) The method of claim 59, wherein said sequence having at least 85% sequence identity to a complement of SEQ ID NO:1 is at least 500 nucleotides long.

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- 61. (New) The method of claim 17, wherein said isolated polynucleotide comprises a sequence having at least 90% identity to a complement of SEQ ID:1.
- 62. (New) (New) The method of claim 61, wherein said isolated polynucleotide comprises a sequence having at least 95% identity to a complement of SEQ ID:1.
- 63. (New) The method of claim 62, wherein said isolated polynucleotide comprises a sequence having at least 98% identity to a complement of SEQ ID:1.
- 64. (New) The method of claim 36, wherein said sequence having at least 85% sequence identity to a complement of SEQ ID NO:1 is at least 100 nucleotides long.
- 65. (New) The method of claim 64, wherein said sequence having at least 85% sequence identity to a complement of SEQ ID NO:1 is at least 200 nucleotides long.
- 66. (New) The method of claim 65, wherein said sequence having at least 85% sequence identity to a complement of SEQ ID NO:1 is at least 500 nucleotides long.
- 67. (New) The method of claim 36, wherein said isolated polynucleotide comprises a sequence having at least 90% identity to a complement of SEQ ID:1.
- 68. (New) (New) The method of claim 67, wherein said isolated polynucleotide comprises a sequence having at least 95% identity to a complement of SEQ ID:1.
- 69. (New) The method of claim 68, wherein said isolated polynucleotide comprises a sequence having at least 98% identity to a complement of SEQ ID:1.

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- 70. (New) The method of claim 37, wherein said sequence having at least 85% sequence identity to a complement of SEQ ID NO:1 is at least 100 nucleotides long.
- 71. (New) The method of claim 70, wherein said sequence having at least 85% sequence identity to a complement of SEQ ID NO:1 is at least 200 nucleotides long.
- 72. (New) The method of claim 71, wherein said sequence having at least 85% sequence identity to a complement of SEQ ID NO:1 is at least 500 nucleotides long.
- 73. (New) The method of claim 37, wherein said isolated polynucleotide comprises a sequence having at least 90% identity to a complement of SEQ ID:1.
- 74. (New) (New) The method of claim 73, wherein said isolated polynucleotide comprises a sequence having at least 95% identity to a complement of SEQ ID:1.
- 75. (New) The method of claim 74, wherein said isolated polynucleotide comprises a sequence having at least 98% identity to a complement of SEQ ID:1.
- 76. (New) The method of claim 17, wherein said control element is a tissue-specific promoter.
- 77. (New) The method of claim 17, wherein said control element directs expression in the vegetative tissue of a plant.
- 78. (New) The method of claim 65, wherein said vegetative tissue is root tissue.
- 79. (New) The method of claim 65, wherein said vegetative tissue is a shoot tissue.

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(New) The method of claim 65, wherein said vegetative tissue is leaf tissue. 80.